Study of S Gene Mutation in Chronic HBV Patients from Golestan Provience- Iran

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Background & Objectives: Mutations of HBsAg especially within the ‘‘a’’determinant could alter the antigenicity of the protein causing failure of HBsAg neutralization and escaping from the host’s immune system. This project aimed to investigate mutation in the S gene region of HBV infected patients in Golestan Province-Iran.

Methods: HBV-DNA extractions from plasma and PCR of 100 patients were performed. Direct sequencing and alignment of S gene were applied using reference sequence from Gene Bank database.

Results: All isolates were belonged to genotype D, subgenotype D1, subtype ayw2. Overall 92 point mutations occurred. Of them, 40 (43.47%) were missense and 52 (56.52%) were silent. Mutations were detected in 95 cases (95%). Five of 40 mutations (12.5%) occurred in ‘‘a’’ determinant and 13 (32.5%), 17 (42.5%), and 2 (5%) were seen in antigenic epitope regions of B cell, CD4 and CTL, respectively. Frame shift mutations were seen in 22 cases (22%). 14% of mutations occurred at Major Hydrophilic Region(MHR) area which P120T/S and R122K/T substitutions were the most frequent ones (4%). Mutation in G145R of the S gene was observed in one case.

Conclusion: This study showed ‘‘a’’ determinant S gene mutations in HBV infected people with HBsAg positivity in Golestan Province-Iran. Collectively, the results of this project exhibited that most of mutations were clustered in CD4 antigenic epitopes.

Keywords: HBV; S Gene; Mutation; Golestan, Iran